

OIPE

RAW SEQUENCE LISTING

DATE: 05/21/2001

PATENT APPLICATION: US/09/851,673

TIME: 09:59:12

Input Set : A:\3198 Seq Listing 050801.txt

Output Set: N:\CRF3\05212001\I851673.raw

ENTERED

3 <110> APPLICANT: Derry, Jonathan
 4 Fanslow, William
 5 Dougall, William
 7 <120> TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
 9 <130> FILE REFERENCE: 3198
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/851,673
 12 <141> CURRENT FILING DATE: 2001-05-08
 14 <160> NUMBER OF SEQ ID NOS: 4
 16 <170> SOFTWARE: PatentIn version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1994
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (149)..(1405)
 27 <400> SEQUENCE: 1

28	ggcagcagca tggcccttgt gatccaggtg gggaaactaa ggcccagaga agtgaggacc	60
30	ccgcagacta tcaatcccag tctcttcccc tcaactccctg tgaagctctc cagcatcatc	120
32	gaggtcccat cagcccttgc cctgttgg atg aat agg cac ctc tgg aag agc	172
33	Met Asn Arg His Leu Trp Lys Ser	
34	1 5	
36	caa ctg tgt gag atg gtg cag ccc agt ggt ggc ccg gca gca gat cag	220
37	Gln Leu Cys Glu Met Val Gln Pro Ser Gly Gly Pro Ala Ala Asp Gln	
38	10 15 20	
40	gac gta ctg ggc gaa gag tct cct ctg ggg aag cca gcc atg ctg cac	268
41	Asp Val Leu Gly Glu Glu Ser Pro Leu Gly Lys Pro Ala Met Leu His	
42	25 30 35 40	
44	ctg cct tca gaa cag ggc gct cct gag acc ctc cag cgc tgc ctg gag	316
45	Leu Pro Ser Glu Gln Gly Ala Pro Glu Thr Leu Gln Arg Cys Leu Glu	
46	45 50 55	
48	gag aat caa gag ctc cga gat gcc atc cgg cag agc aac cag att ctg	364
49	Glu Asn Gln Glu Leu Arg Asp Ala Ile Arg Gln Ser Asn Gln Ile Leu	
50	60 65 70	
52	cgg gag cgc tgc gag gag ctt ctg cat ttc caa gcc agc cag agg gag	412
53	Arg Glu Arg Cys Glu Glu Leu Leu His Phe Gln Ala Ser Gln Arg Glu	
54	75 80 85	
56	gag aag gag ttc ctc atg tgc aag ttc cag gag gcc agg aaa ctg gtg	460
57	Glu Lys Glu Phe Leu Met Cys Lys Phe Gln Glu Ala Arg Lys Leu Val	
58	90 95 100	
60	gag aga ctc ggc ctg gag aag ctc gat ctg aag agg cag aag gag cag	508
61	Glu Arg Leu Gly Leu Glu Lys Leu Asp Leu Lys Arg Gln Lys Glu Gln	
62	105 110 115 120	
64	gct ctg cgg gag gtg gag cac ctg aag aga tgc cag cag cag atg gct	556
65	Ala Leu Arg Glu Val Glu His Leu Lys Arg Cys Gln Gln Gln Met Ala	
66	125 130 135	
68	gag gac aag gcc tct gtg aaa gcc cag gtg acg tcc ttg ctc ggg gag	604

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69 Glu Asp Lys Ala Ser Val Lys Ala Gln Val Thr Ser Leu Leu Gly Glu
70      140      145      150
72 ctg cag gag agc cag agt cgc ttg gag gct gcc act aag gaa tgc cag      652
73 Leu Gln Glu Ser Gln Ser Arg Leu Glu Ala Ala Thr Lys Glu Cys Gln
74      155      160      165
76 gct ctg gag ggt cgg gcc cgg gcg gcc agc gag cag gcg cgg cag ctg      700
77 Ala Leu Glu Gly Arg Ala Arg Ala Ala Ser Glu Gln Ala Arg Gln Leu
78      170      175      180
80 gag agt gag cgc gag gcg ctg cag cag cag cac agc gtg cag gtg gac      748
81 Glu Ser Glu Arg Glu Ala Leu Gln Gln Gln His Ser Val Gln Val Asp
82 185      190      195      200
84 cag ctg cgc atg cag ggc cag agc gtg gag gcc gcg ctc cgc atg gag      796
85 Gln Leu Arg Met Gln Gly Gln Ser Val Glu Ala Ala Leu Arg Met Glu
86      205      210      215
88 cgc cag gcc gcc tcg gag gag aag agg aag ctg gcc cag ttg cag gtg      844
89 Arg Gln Ala Ala Ser Glu Glu Lys Arg Lys Leu Ala Gln Leu Gln Val
90      220      225      230
92 gcc tat cac cag ctc ttc caa gaa tac gac aac cac atc aag agc agc      892
93 Ala Tyr His Gln Leu Phe Gln Glu Tyr Asp Asn His Ile Lys Ser Ser
94      235      240      245
96 gtg gtg ggc agt gag cgg aag cga gga atg cag ctg gaa gat ctc aaa      940
97 Val Val Gly Ser Glu Arg Lys Arg Gly Met Gln Leu Glu Asp Leu Lys
98      250      255      260
100 cag cag ctc cag cag gcc gag gag gcc ctg gtg gcc aaa cag gag gtg      988
101 Gln Gln Leu Gln Gln Ala Glu Glu Ala Leu Val Ala Lys Gln Glu Val
102 265      270      275      280
104 atc gat aag ctg aag gag gag gcc gag cag cac aag att gtg atg gag      1036
105 Ile Asp Lys Leu Lys Glu Glu Ala Glu Gln His Lys Ile Val Met Glu
106      285      290      295
108 acc gtt ccg gtg ctg aag gcc cag gcg gat atc tac aag gcg gac ttc      1084
109 Thr Val Pro Val Leu Lys Ala Gln Ala Asp Ile Tyr Lys Ala Asp Phe
110      300      305      310
112 cag gct gag agg cag gcc cgg gag aag ctg gcc gag aag aag gag ctc      1132
113 Gln Ala Glu Arg Gln Ala Arg Glu Lys Leu Ala Glu Lys Lys Glu Leu
114      315      320      325
116 ctg cag gag cag ctg gag cag ctg cag agg gag tac agc aaa ctg aag      1180
117 Leu Gln Glu Gln Leu Glu Gln Leu Gln Arg Glu Tyr Ser Lys Leu Lys
118      330      335      340
120 gcc agc tgt cag gag tcg gcc agg atc gag gac atg agg aag cgg cat      1228
121 Ala Ser Cys Gln Glu Ser Ala Arg Ile Glu Asp Met Arg Lys Arg His
122 345      350      355      360
124 gtc gag gtc tcc cag gcc ccc ttg ccc ccc gcc cct gcc tac ctc tcc      1276
125 Val Glu Val Ser Gln Ala Pro Leu Pro Pro Ala Pro Ala Tyr Leu Ser
126      365      370      375
128 tct ccc ctg gcc ctg ccc agc cag agg agg agc ccc ccc gag gag cca      1324
129 Ser Pro Leu Ala Leu Pro Ser Gln Arg Arg Ser Pro Pro Glu Glu Pro
130      380      385      390
132 cct gac ttc tgc tgt ccc aag tgc cag tat cag gcc cct gat atg gac      1372
133 Pro Asp Phe Cys Cys Pro Lys Cys Gln Tyr Gln Ala Pro Asp Met Asp

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134          395          400          405
136 acc ctg cag ata cat gtc atg gag tgc att gag tagggccggc cagtgcgaagg 1425
137 Thr Leu Gln Ile His Val Met Glu Cys Ile Glu
138          410          415
140 ccactgcctg cccgaggacg tgcgggggac cgtgcagtct gcgctttcct ctcccgccctg 1485
142 cctagcccag gatgaagggc tgggtggcca caactgggat gccacctgga gccccaccca 1545
144 ggagctggcc gcgcacctt acgcttcagc tgttgatccg ctgggtccct cttttgggggt 1605
146 agatgcggcc ccgatcaggc ctgactcgct gctctttttg ttccctctctg tctgctcgaa 1665
148 ccacttgccct cgggctaate cctccctctt cctccaccgc gcactgggga agtcaagaat 1725
150 ggggcctggg gctctcaggc agaactgctt cccctggcag agctgggtgg cagctcttcc 1785
152 tcccaccgga caccgacccg ccgcgcgctg tgccctggga gtgctgccct cttaccatgc 1845
154 acacgggtgc tctccttttg ggctgcatgc tattccattt tgcagccaga ccgatgtgta 1905
156 tttaaccagt cactattgat ggacatttgg gttgtttccc atctttttgt taccataaat 1965
158 aatggcatag taaaaaaaaa aaaaaaaaaa 1994
161 <210> SEQ ID NO: 2
162 <211> LENGTH: 419
163 <212> TYPE: PRT
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 2
168 Met Asn Arg His Leu Trp Lys Ser Gln Leu Cys Glu Met Val Gln Pro
169 1 5 10 15
172 Ser Gly Gly Pro Ala Ala Asp Gln Asp Val Leu Gly Glu Glu Ser Pro
173 20 25 30
176 Leu Gly Lys Pro Ala Met Leu His Leu Pro Ser Glu Gln Gly Ala Pro
177 35 40 45
180 Glu Thr Leu Gln Arg Cys Leu Glu Glu Asn Gln Glu Leu Arg Asp Ala
181 50 55 60
184 Ile Arg Gln Ser Asn Gln Ile Leu Arg Glu Arg Cys Glu Glu Leu Leu
185 65 70 75 80
188 His Phe Gln Ala Ser Gln Arg Glu Glu Lys Glu Phe Leu Met Cys Lys
189 85 90 95
192 Phe Gln Glu Ala Arg Lys Leu Val Glu Arg Leu Gly Leu Glu Lys Leu
193 100 105 110
196 Asp Leu Lys Arg Gln Lys Glu Gln Ala Leu Arg Glu Val Glu His Leu
197 115 120 125
200 Lys Arg Cys Gln Gln Gln Met Ala Glu Asp Lys Ala Ser Val Lys Ala
201 130 135 140
204 Gln Val Thr Ser Leu Leu Gly Glu Leu Gln Glu Ser Gln Ser Arg Leu
205 145 150 155 160
208 Glu Ala Ala Thr Lys Glu Cys Gln Ala Leu Glu Gly Arg Ala Arg Ala
209 165 170 175
212 Ala Ser Glu Gln Ala Arg Gln Leu Glu Ser Glu Arg Glu Ala Leu Gln
213 180 185 190
216 Gln Gln His Ser Val Gln Val Asp Gln Leu Arg Met Gln Gly Gln Ser
217 195 200 205
220 Val Glu Ala Ala Leu Arg Met Glu Arg Gln Ala Ala Ser Glu Glu Lys
221 210 215 220
224 Arg Lys Leu Ala Gln Leu Gln Val Ala Tyr His Gln Leu Phe Gln Glu
225 225 230 235 240

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228 Tyr Asp Asn His Ile Lys Ser Ser Val Val Gly Ser Glu Arg Lys Arg
229                245                250                255
232 Gly Met Gln Leu Glu Asp Leu Lys Gln Gln Leu Gln Gln Ala Glu Glu
233                260                265                270
236 Ala Leu Val Ala Lys Gln Glu Val Ile Asp Lys Leu Lys Glu Glu Ala
237                275                280                285
240 Glu Gln His Lys Ile Val Met Glu Thr Val Pro Val Leu Lys Ala Gln
241                290                295                300
244 Ala Asp Ile Tyr Lys Ala Asp Phe Gln Ala Glu Arg Gln Ala Arg Glu
245 305                310                315                320
248 Lys Leu Ala Glu Lys Lys Glu Leu Leu Gln Glu Gln Leu Glu Gln Leu
249                325                330                335
252 Gln Arg Glu Tyr Ser Lys Leu Lys Ala Ser Cys Gln Glu Ser Ala Arg
253                340                345                350
256 Ile Glu Asp Met Arg Lys Arg His Val Glu Val Ser Gln Ala Pro Leu
257                355                360                365
260 Pro Pro Ala Pro Ala Tyr Leu Ser Ser Pro Leu Ala Leu Pro Ser Gln
261                370                375                380
264 Arg Arg Ser Pro Pro Glu Glu Pro Pro Asp Phe Cys Cys Pro Lys Cys
265 385                390                395                400
268 Gln Tyr Gln Ala Pro Asp Met Asp Thr Leu Gln Ile His Val Met Glu
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272 Cys Ile Glu
276 <210> SEQ ID NO: 3
277 <211> LENGTH: 5371
278 <212> TYPE: DNA
279 <213> ORGANISM: Homo sapiens
281 <220> FEATURE:
282 <221> NAME/KEY: CDS
283 <222> LOCATION: (392)..(3262)
285 <400> SEQUENCE: 3
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288 ttctagggtg aggatggttc tacacagcca cccggagttc cttagttgaa aggtgcgccc      120
290 tgctgtgaca gaatgtggtg attgtaattt ttaacatttt catgtaaaac atatttcctg      180
292 atcatctttc cattgtcttc atggaaaatt gataaatatt tgtgccttcc aactctcgtc      240
294 ttggttgaat gacttcattc taatacaaca tggacaccac gttgctgaaa acatgctttg      300
296 ggactgccac tgaatttata ttttgcggtt ttatgacaaa gttattagta gtttcccttt      360
298 tttgaattag tattttgaag ttaatatcac a atg agt tca ggc tta tgg agc      412
299                Met Ser Ser Gly Leu Trp Ser
300                1                5
302 caa gaa aaa gtc act tca ccc tac tgg gaa gag cgg att ttt tac ttg      460
303 Gln Glu Lys Val Thr Ser Pro Tyr Trp Glu Glu Arg Ile Phe Tyr Leu
304                10                15                20
306 ctt ctt caa gaa tgc agc gtt aca gac aaa caa aca caa aag ctc ctt      508
307 Leu Leu Gln Glu Cys Ser Val Thr Asp Lys Gln Thr Gln Lys Leu Leu
308                25                30                35
310 aaa gta ccg aag gga agt ata gga cag tat att caa gat cgt tct gtg      556
311 Lys Val Pro Lys Gly Ser Ile Gly Gln Tyr Ile Gln Asp Arg Ser Val
312 40                45                50                55

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314 ggg cat tca agg att cct tct gca aaa ggc aag aaa aat cag att gga      604
315 Gly His Ser Arg Ile Pro Ser Ala Lys Gly Lys Lys Asn Gln Ile Gly
316              60              65              70
318 tta aaa att cta gag caa cct cat gca gtt ctc ttt gtt gat gaa aag      652
319 Leu Lys Ile Leu Glu Gln Pro His Ala Val Leu Phe Val Asp Glu Lys
320              75              80              85
322 gat gtt gta gag ata aat gaa aag ttc aca gag tta ctt ttg gca att      700
323 Asp Val Val Glu Ile Asn Glu Lys Phe Thr Glu Leu Leu Leu Ala Ile
324              90              95              100
326 acc aat tgt gag gag agg ttc agc ctg ttt aaa aac aga aac aga cta      748
327 Thr Asn Cys Glu Glu Arg Phe Ser Leu Phe Lys Asn Arg Asn Arg Leu
328      105              110              115
330 agt aaa ggc ctc caa ata gac gtg ggc tgt cct gtg aaa gta cag ctg      796
331 Ser Lys Gly Leu Gln Ile Asp Val Gly Cys Pro Val Lys Val Gln Leu
332 120              125              130              135
334 aga tct ggg gaa gaa aaa ttt cct gga gtt gta cgc ttc aga gga ccc      844
335 Arg Ser Gly Glu Glu Lys Phe Pro Gly Val Val Arg Phe Arg Gly Pro
336              140              145              150
338 ctg tta gca gag agg aca gtc tcc gga ata ttc ttt gga gtt gaa ttg      892
339 Leu Leu Ala Glu Arg Thr Val Ser Gly Ile Phe Phe Gly Val Glu Leu
340              155              160              165
342 ctg gaa gaa ggt cgt ggt caa ggt ttc act gac ggg gtg tac caa ggg      940
343 Leu Glu Glu Gly Arg Gly Gln Gly Phe Thr Asp Gly Val Tyr Gln Gly
344              170              175              180
346 aaa cag ctt ttt cag tgt gat gaa gat tgt ggc gtg ttt gtt gca ttg      988
347 Lys Gln Leu Phe Gln Cys Asp Glu Asp Cys Gly Val Phe Val Ala Leu
348      185              190              195
350 gac aag cta gaa ctc ata gaa gat gat gac act gca ttg gaa agt gat      1036
351 Asp Lys Leu Glu Leu Ile Glu Asp Asp Asp Thr Ala Leu Glu Ser Asp
352 200              205              210              215
354 tac gca ggt cct ggg gac aca atg cag gtc gaa ctt cct cct ttg gaa      1084
355 Tyr Ala Gly Pro Gly Asp Thr Met Gln Val Glu Leu Pro Pro Leu Glu
356              220              225              230
358 ata aac tcc aga gtt tct ttg aag gtt gga gaa aca ata gaa tct gga      1132
359 Ile Asn Ser Arg Val Ser Leu Lys Val Gly Glu Thr Ile Glu Ser Gly
360              235              240              245
362 aca gtt ata ttc tgt gat gtt ttg cca gga aaa gaa agc tta gga tat      1180
363 Thr Val Ile Phe Cys Asp Val Leu Pro Gly Lys Glu Ser Leu Gly Tyr
364              250              255              260
366 ttt gtt ggt gtg gac atg gat aac cct att ggc aac tgg gat gga aga      1228
367 Phe Val Gly Val Asp Met Asp Asn Pro Ile Gly Asn Trp Asp Gly Arg
368      265              270              275
370 ttt gat gga gtg cag ctt tgt agt ttt gcg tgt gtt gaa agt aca att      1276
371 Phe Asp Gly Val Gln Leu Cys Ser Phe Ala Cys Val Glu Ser Thr Ile
372 280              285              290              295
374 cta ttg cac atc aat gat atc atc cca gct tta tca gag agt gtg acg      1324
375 Leu Leu His Ile Asn Asp Ile Ile Pro Ala Leu Ser Glu Ser Val Thr
376              300              305              310
378 cag gaa agg agg cct ccc aaa ctt gcc ttt atg tca aga ggt gtt ggg      1372

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VERIFICATION SUMMARY

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Input Set : A:\3198 Seq Listing 050801.txt

Output Set: N:\CRF3\05212001\I851673.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number